



Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

Cuellar, Ana Carolina; Schou, Kirstine Klitgaard; Moutailler, Sara; Fach, Patrick; Delannoy, Sabine; van der Wal, Fimme Jan; de Koeier, Aline; Chirico, Jan; Aspán, Anna; Juremalm, Mikael

Total number of authors:
14

Publication date:
2016

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Cuellar, A. C. (Author), Schou, K. K. (Author), Moutailler, S. (Author), Fach, P. (Author), Delannoy, S. (Author), van der Wal, F. J. (Author), de Koeier, A. (Author), Chirico, J. (Author), Aspán, A. (Author), Juremalm, M. (Author), Mansfield, K. (Author), Phipps, P. (Author), Fooks, T. (Author), & Bødker, R. (Author). (2016). Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe. Sound/Visual production (digital), Technical University of Denmark.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

Ana Carolina Cuellar, Kirstine Klitgaard Schou, Sara Moutailler, Patrick Fach, Sabine Delannoy, Fimme van der Wal, Aline de Koeier, Jan Chirico, Anna Aspán, Mikael Juremalm, Karen Mansfield, Paul Phipps, Tony Fooks and Rene Bødker



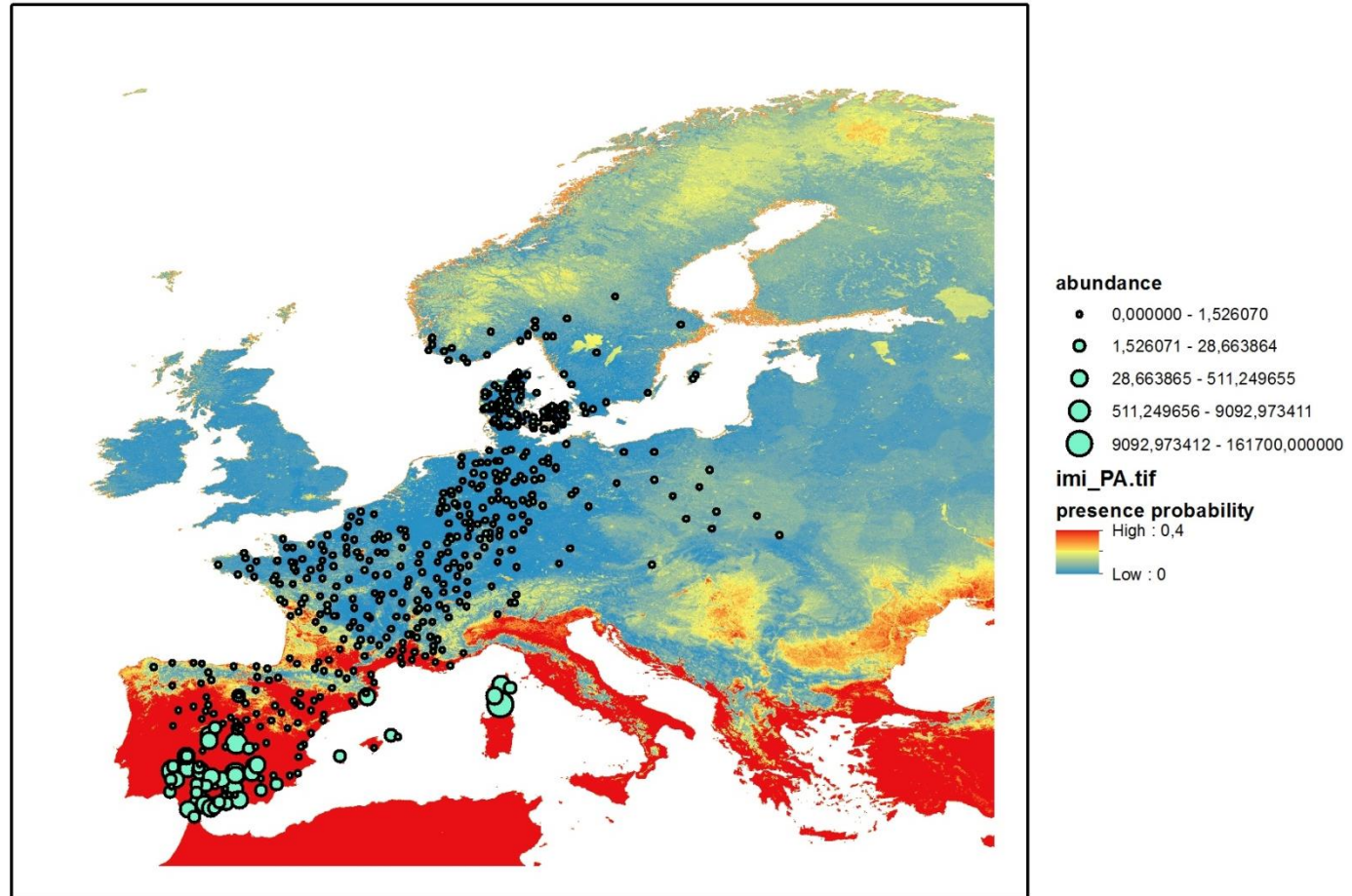
Founded by CoVetLab and InterReg

Introduction

Abstraktion of reality  **Modelling**  Predictions, planning



Culicioides imicola suitability map



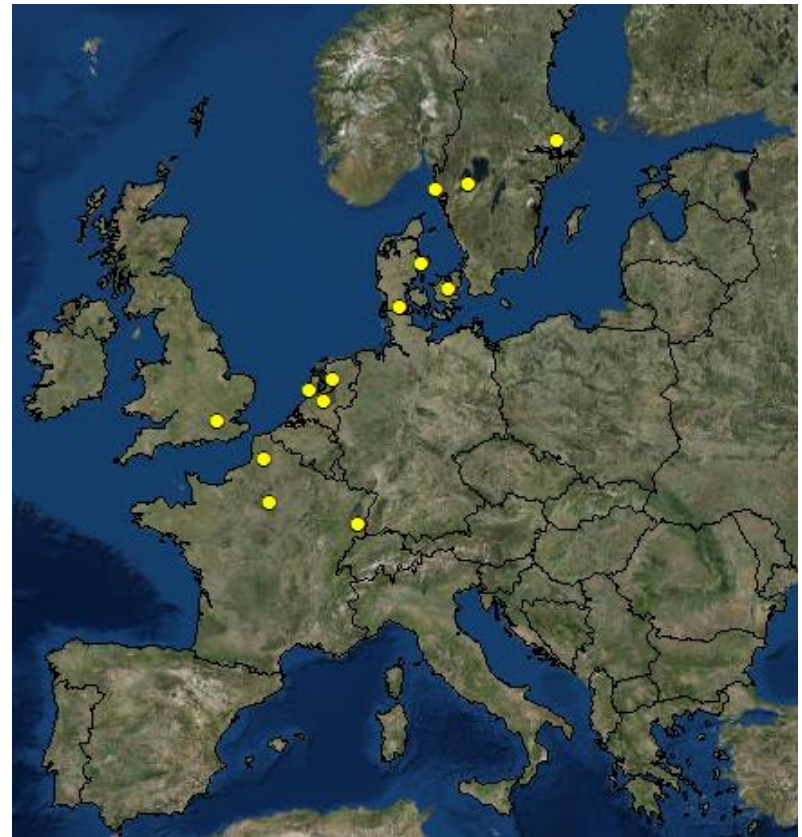
Methods and materials

16000 ticks
(*Ixodes ricinus*)

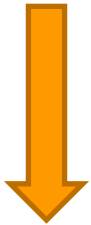


49 pools of 25 nymphs, per site

13 locations (England, Sweden, Denmark,
Netherlands and France)



Pathogen detection (PCR techniques)



Pooled prevalence for fixed pool size and perfect tests

Pathogen prevalence

We use:

five species of Bacteria:

- *Borrelia Burgdorferi*
- *Borrelia Garinii*
- *Borrelia Miyamotoi*
- *Anaplasma phagocytophilum*
- *Candidatus N. mikurensis*

two species of parasites

- *Babesia divergens*
- *Babesia venatorum* (sp. EU1)



Data analysis

Machine learning techniques:

- Data drawn from unknown distribution, black box
- Predictive accuracy

Random Forest

Statistical analysis:

- Known data distribution
- P-value, confidence intervals

90 predictors: Remote sensing imagery (1km)

70 Fourier processed MODIS imagery:

- LST day
- LST night
- NDVI
- EVI



Modis: mean day temperature

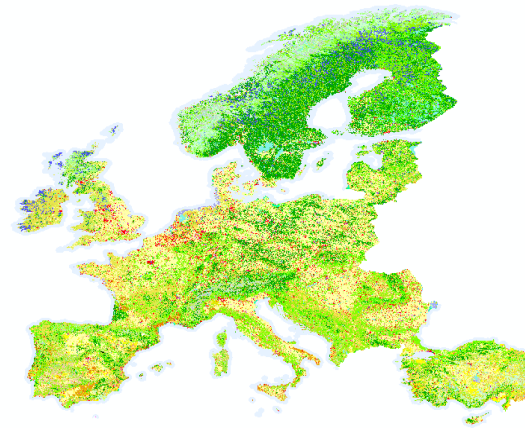
Worldclim: mean precipitation



-19 Worldclim imagery:

- Temperature and precipitation

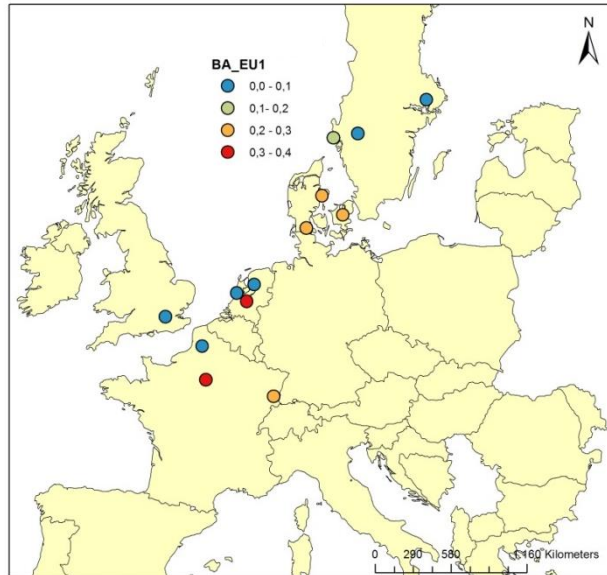
Corine Land Cover:



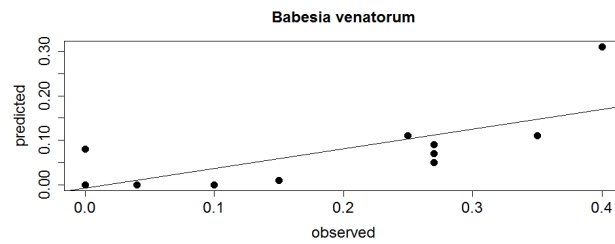
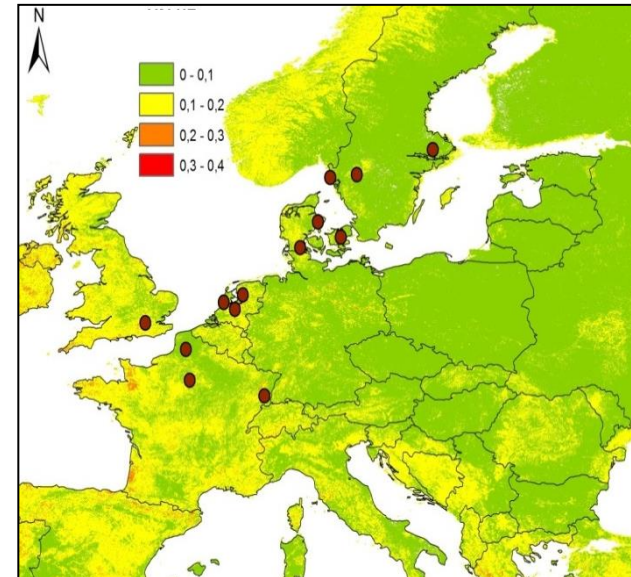
Results

Babesia venatorum

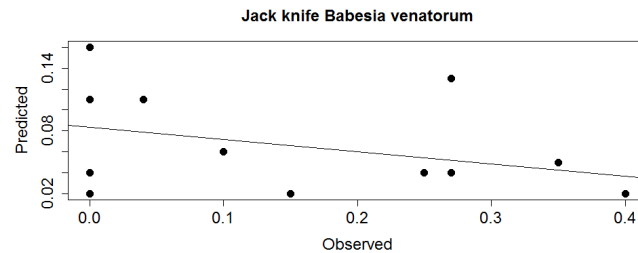
%Prevalence



Probability of presence



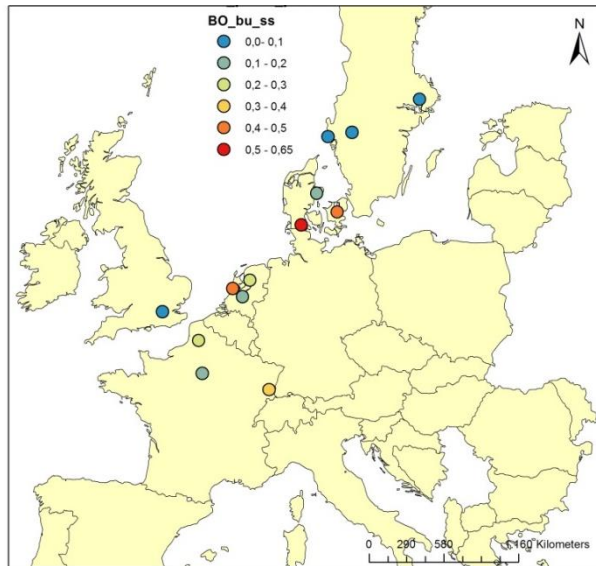
$P=0.003089$



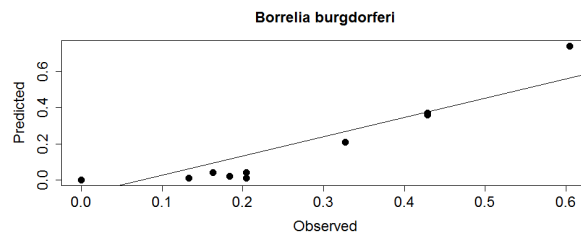
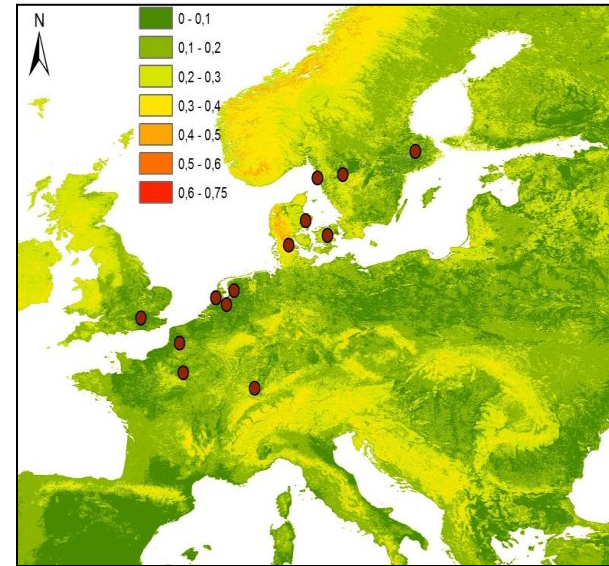
$P=0.2185$

Borrelia burgdorferi

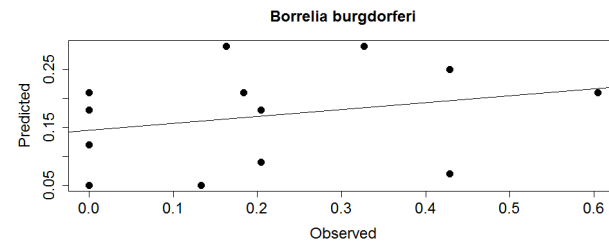
%Prevalence



Probability of presence

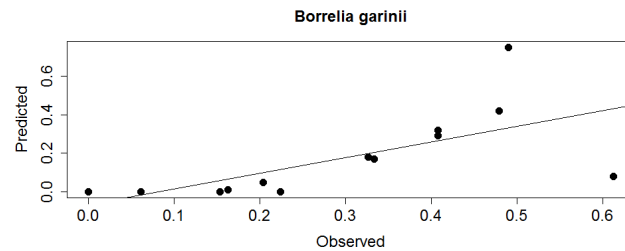
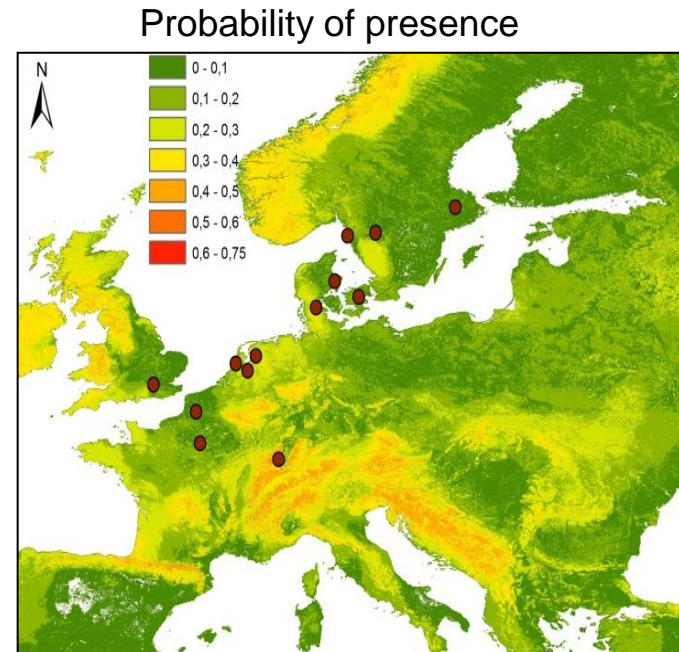
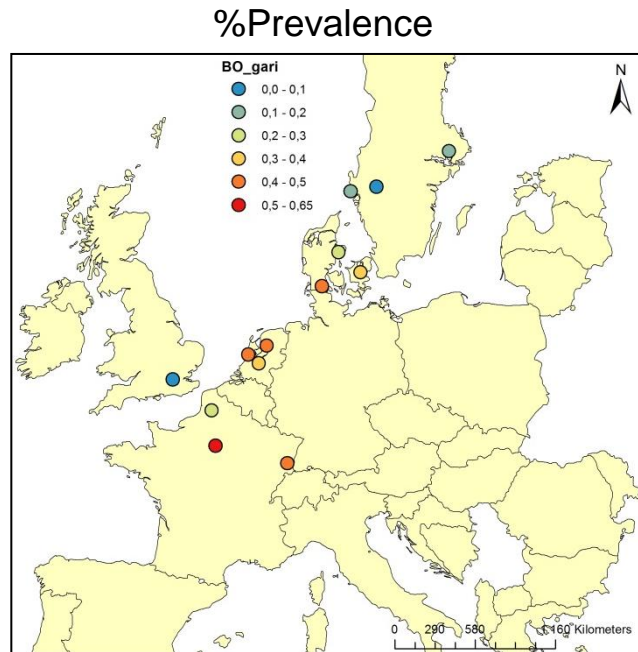


$P < 0.001$

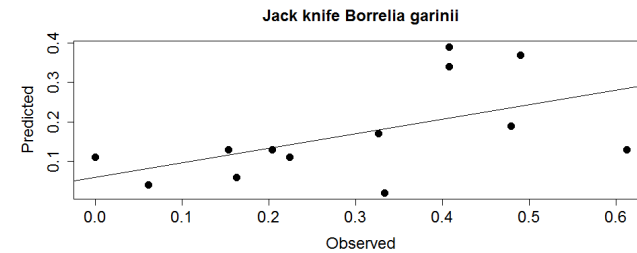


$P = 0.3739$

Borrelia garinii

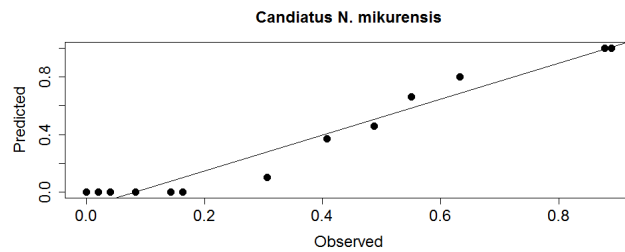
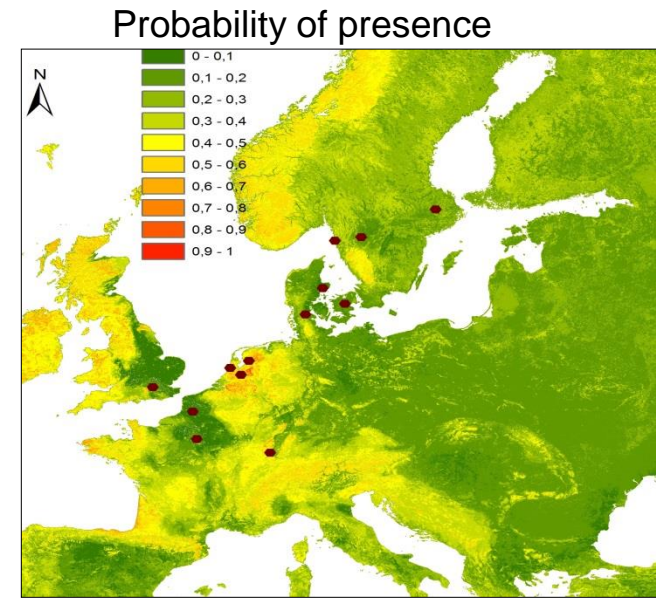
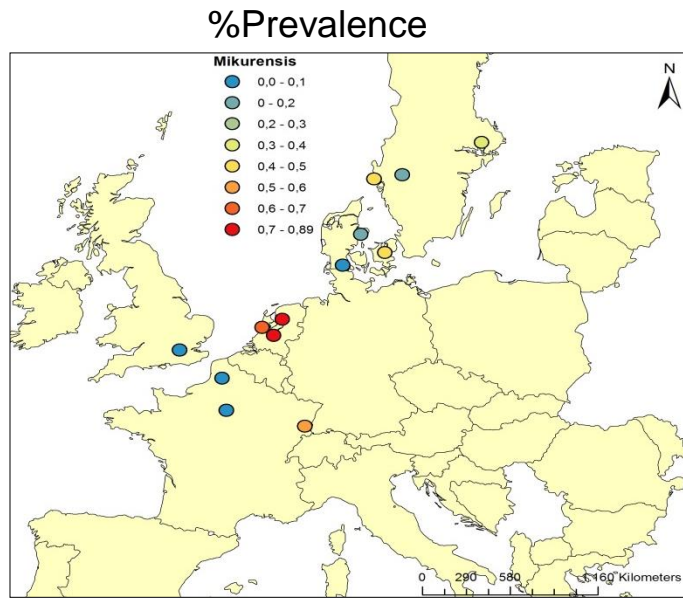


P=0,01456

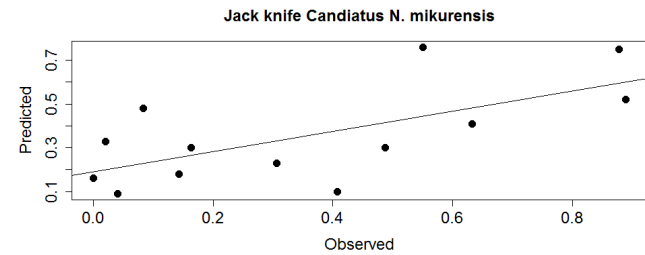


P=0,05589

Candidatus *Neoehrlichia mikereensis*



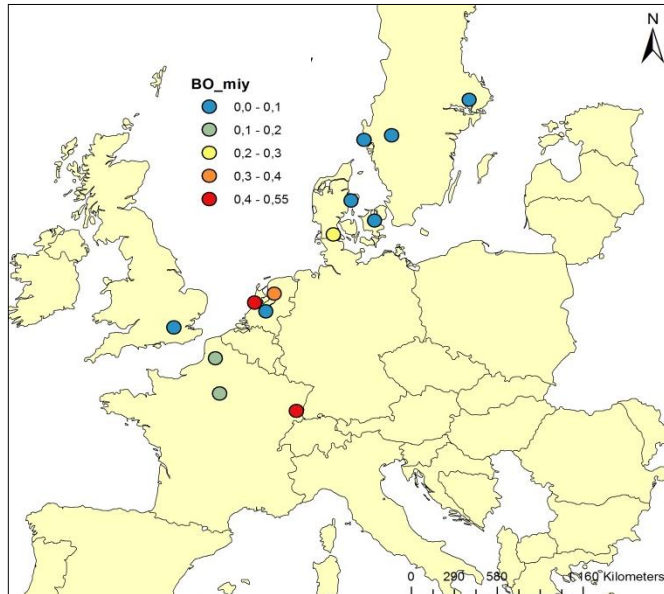
$P < 0,001$



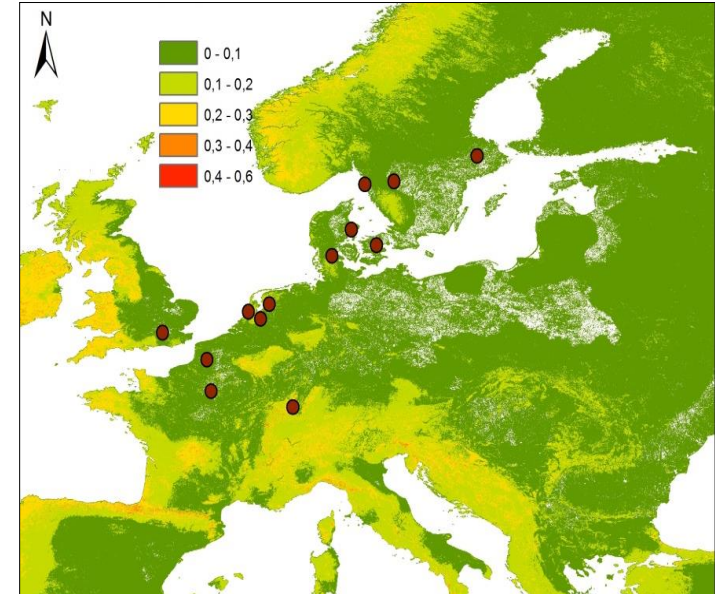
$P = 0,01523$

Borrelia miyamotoi

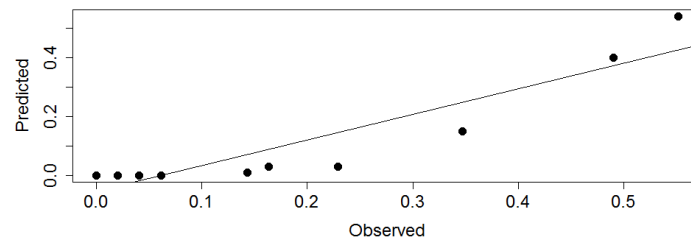
%Prevalence



Probability of presence

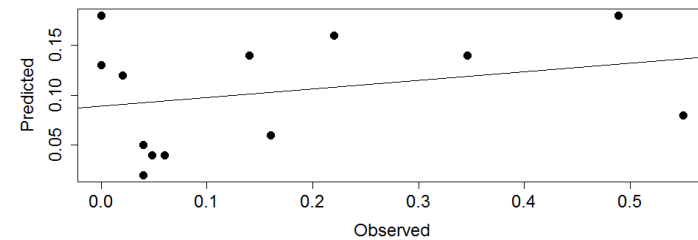


Borrelia miyamotoi



$p < 0,001$

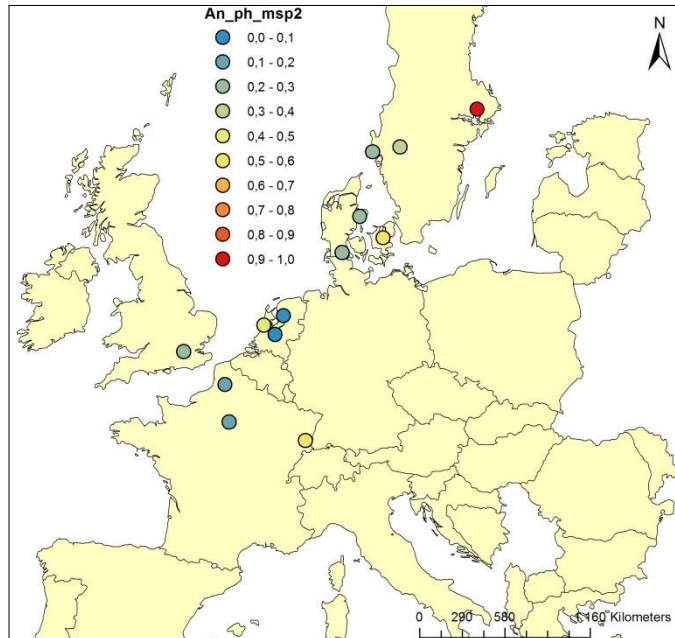
Jack knife *Borrelia miyamotoi*



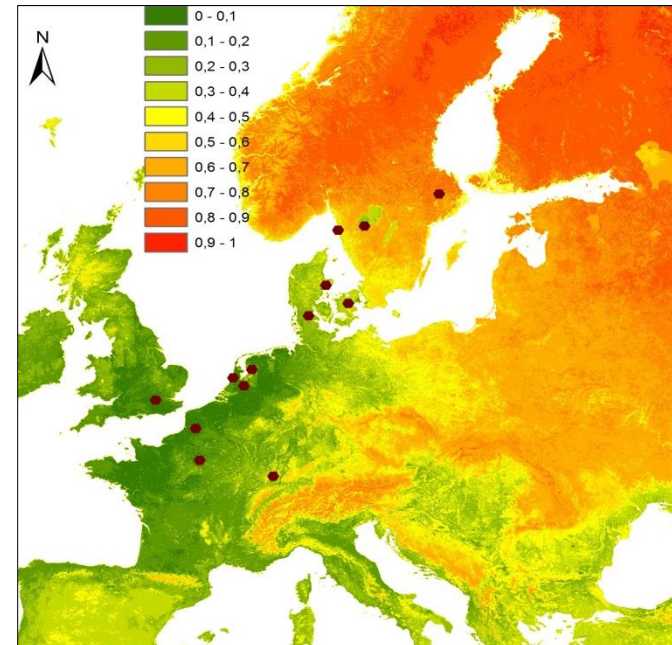
$P = 0.3436$

Anaplasma phagocytophilum

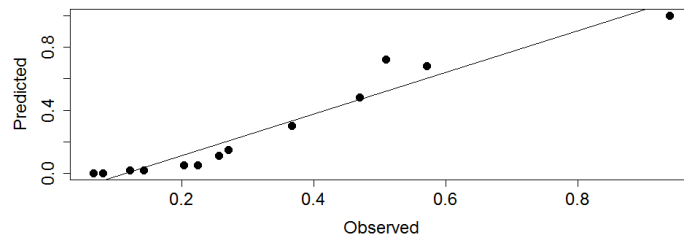
%Prevalence



Probability of presence

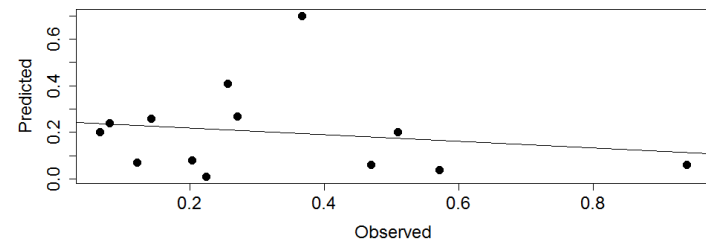


Anaplasma phagocytophilum



$P < 0,001$

Anaplasma phagocytophilum



$P = 0.5486$

Discussion/conclusion

- Pathogens prevalence differ between sites
- First attempt to model tick pathogens using environmental variables from remote sensing data
- Observed prevalences fit the environmental data 😊
- Overfitting: few observations
- Other algorithms like Boosted Regression Trees

**Thank you
for your attention**

Ana Carolina Cuellar
anacu@vet.dtu.dk